

SEQ ID NO. 17

1 CCCTTTAAAG AGGGCTTTTA TATATTAATC ACAAATCACT TATCACAAAT
 51 CACAAGTGAT TTGTGATTGT TGATGATAAA ATAAGAATAA GAAGAAATAG
 101 AAAGAAGTGA GTGATTGTGG GAAATTTAGG CGCACAAAAA GAAAGAGTGT
 -35
 151 GACAAAACAT GGTTATGCTA CATGTTTAAG GTAAAAATAG TTATGTCACA
 -10
 201 ACTACTTATT TTTTACCCA ATCTTCTAGA CTATAATTAA AATTAAATAA

XbaI

M T I P D A N A I Y

251 CTCAATTCCG AGGTACTAAC ATGACTATAC CTGACGCAA TGCAATCTAT

SEQ ID NO. 18

RBS

START

H N S A I K E V V F I K N V I K S
 301 CATAACTCAG CCATCAAAGA GGTGTCTTT ATCAAGAACG TGATCAAAAG

DdeI

DpnI

P N I E I G D Y T Y Y D D P V N
 351 TCCCAATATT GAAATTGGGG ACTACACCTA TTATGATGAC CCAGTAAATC

SspI

P T D F E K H V T H H Y E F L G D
 401 CCACCGATTT TGAGAAACAC GTTACCCATC ACTATGAATT TCTAGGCGAC

K L I I G K F C S L A S G I E F I
 451 AAATTAATCA TCGGTAAATT TTGTTCTCTC GCCAGTGGCA TTGAATTTAT

M N G A N H V M K G I S T Y P F
 501 CATGAACGGT GCCAACCACG TAATGAAAGG TATTTCGACT TATCCATTTA

TaqI

N I L G G D W Q Q Y T P E L T D L
 551 ATATATTAGG TGGCGATTGG CAACAATACA CTCCTGAACT GACTGATTTG

P L K G T V V G N D V W F G Q N V
 601 CCGTTGAAAG GTGATACTGT AGTCGGAAAT GACGTGTGGT TTGGGCAAAA

T V L P G V K I G D G A I I G A
 651 TGTGACCGTC CTACCAGGCG TAAAAATAGG TGACGGTGCC ATTATCGGAG

N S V V T K D V A P Y T I V G G N
 701 CAAATAGTGT TGTAACAAAA GACGTCGCTC CATATACAAT TGTCGGTGGC

P I Q L I G P R F E P E V I Q A L
 751 AATCCAATTC AACTCATCGG ACCAAGATTT GAACCGGAAG TTATTCAAGC

XmnI

E N L A W W N K D I E W I T A N
 801 ATTAGAAAAT CTGGCATGGT GGAATAAAGA TATTGAATGG ATAAGTCTA

N V P K L M Q T T P T L E L I N S
 851 ATGTTCTCTAA ACTAATGCAA ACAACACCCA CACTTGAATT GATAAACAGT

L M E K *

STOP

901 TTAATGGAAA AATAAAAAACA AAAAAGCCGT GCAAGCAATC CAAAAATGAT
 951 TGTTTACACG GCCTTTACTA TTTAGTGAAT CCAATTTATT AATAATAGAT

HaeIII

1001 ATGATATACC AGTAAAAAAT AACTAGCCA CCTCTGGCGG TACTCTACTC
 1051 GTATATTTTA TTTACGACCT TCTGATGATA

FIGURE 1

Vat
VatC
SatA
VatB
VatD

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1. Introduction

[illegible]

FIGURE3